PCT

RAW SEQUENCE LISTING   DATE: 10/27/2004
PATENT APPLICATION: US/10/511,657   TIME: 15:26:56

.Input Set· : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\10272004\J511657.raw**

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      3 <110> APPLICANT: Lynkeus Biotech GmbH
      5 <120> TITLE OF INVENTION: Means and Methods for the Specific Modulation of Target
Genes in the CNS
      6       and the Eye and Methods for Their Identification
W-->  7 <130> FILE REFERENCE: LY01A04/P-WO
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/511,657
C-->  9 <141> CURRENT FILING DATE: 2004-10-18
      9 <150> PRIOR APPLICATION NUMBER: EP02008761.5
     10 <151> PRIOR FILING DATE: 2002-04-18
     12 <150> PRIOR APPLICATION NUMBER: US 60/431,173
     13 <151> PRIOR FILING DATE: 2002-12-05
     15 <160> NUMBER OF SEQ ID NOS: 10
     17 <170> SOFTWARE: PatentIn version 3.1
     19 <210> SEQ ID NO: 1
     20 <211> LENGTH: 2500
     21 <212> TYPE: DNA
     22 <213> ORGANISM: homo sapiens
     24 <220> FEATURE:
     25 <221> NAME/KEY: CDS
     26 <222> LOCATION: (25)..(2097)
     27 <223> OTHER.INFORMATION: Homo sapiens cyclic nucleotide gated channel alpha 1
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     32                          Met Lys Leu Ser Met Lys Asn Asn Ile
     33                           1               5
     35 atc aat aca cag cag tct ttt gta acc atg ccc aat gtg att gta cca        99
     36 Ile Asn Thr Gln Gln Ser Phe Val Thr Met Pro Asn Val Ile Val Pro
     37 10              15                  20                  25
     39 gat att gaa aag gaa ata cga agg atg gaa aat gga gca tgc agc tcc       147
     40 Asp Ile Glu Lys Glu Ile Arg Arg Met Glu Asn Gly Ala Cys Ser Ser
     41              30                  35                  40
     43 ttt tct gag gat gat gac agt gcc tat aca tct gaa gaa tca gag aat       195
     44 Phe Ser Glu Asp Asp Asp Ser Ala Tyr Thr Ser Glu Glu Ser Glu Asn
     45              45                  50                  55
     47 gaa aac cct cat gca agg ggt tcc ttt agt tat aag tca ctc aga aag       243
     48 Glu Asn Pro His Ala Arg Gly Ser Phe Ser Tyr Lys Ser Leu Arg Lys
     49          60                  65                  70
     51 gga gga cca tca cag agg gag cag tac ctg cct ggt gcc att gcc att       291
     52 Gly Gly Pro Ser Gln Arg Glu Gln Tyr Leu Pro Gly Ala Ile Ala Ile
     53      75                  80                  85
     55 ttt aat gtg aac aac agc agc aat aag gac cag gaa cca gag gaa aaa       339
     56 Phe Asn Val Asn Asn Ser Ser Asn Lys Asp Gln Glu Pro Glu Glu Lys
     57 90              95                  100                 105
     59 aag aaa aag aaa aaa gaa aag aag agc aag tca gat gat aaa aac gaa       387
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60  Lys Lys Lys Lys Lys Glu Lys Lys Ser Lys Ser Asp Asp Lys Asn Glu
61              110                 115                 120
63  aat aaa aac gac cca gag aag aaa aag aag aaa aag gac aaa gag aag       435
64  Asn Lys Asn Asp Pro Glu Lys Lys'Lys Lys Lys Lys Asp Lys Glu Lys
65              125                 130                 135
67  aaa aag aaa gag gag aaa agc aaa gat aag aaa gaa cac cac aag aaa       483
68  Lys Lys Lys Glu Glu Lys Ser Lys Asp Lys Lys Glu His His Lys Lys
69              140                 145                 150
71  gaa gtt gtg gtt att gat ccc tcg gga aac aca tat tac aac tgg ctg       531
72  Glu Val Val Val Ile Asp Pro Ser Gly Asn Thr Tyr Tyr Asn Trp Leu
73      155                 160                 165
75  ttt tgc atc aca tta cct gtt atg tac aac tgg aca atg gtt att gcc       579
76  Phe Cys Ile Thr Leu Pro Val Met Tyr Asn Trp Thr Met Val Ile Ala
77  170                 175                 180                 185
79  aga gca tgt ttt gat gaa ctt caa tct gat tac cta gaa tat tgg ctc       627
80  Arg Ala Cys Phe Asp Glu Leu Gln Ser Asp Tyr Leu Glu Tyr Trp Leu
81              190                 195                 200
83  att ttg gat tac gta tca gac ata gtc tat tta atc gat atg ttt gta       675
84  Ile Leu Asp Tyr Val Ser Asp Ile Val Tyr Leu Ile Asp Met Phe Val
85              205                 210                 215
87  cga aca agg aca ggt tac cta gaa caa gga ctg ctg gta aag gaa gaa       723
88  Arg Thr Arg Thr Gly Tyr Leu Glu Gln Gly Leu Leu Val Lys Glu Glu
89              220                 225                 230
91  ctt aaa ctc ata aat aaa tat aaa tcc aac ttg caa ttt aaa ctt gat       771
92  Leu Lys Leu Ile Asn Lys Tyr Lys Ser Asn Leu Gln Phe Lys Leu Asp
93      235                 240                 245
95  gtt ctg tca ctg ata cca act gat ttg ctg tat ttt aag tta ggg tgg       819
96  Val Leu Ser Leu Ile Pro Thr Asp Leu Leu Tyr Phe Lys Leu Gly Trp
97  250                 255                 260                 265
99  aac tat cca gaa att aga tta aac agg ttg tta cgg ttc tct cgt atg       867
100 Asn Tyr Pro Glu Ile Arg Leu Asn Arg Leu Leu Arg Phe Ser Arg Met
101                 270                 275                 280
103 ttt gag ttc ttc cag aga aca gaa aca agg aca aac tat cca aac atc       915
104 Phe Glu Phe Phe Gln Arg Thr Glu Thr Arg Thr Asn Tyr Pro Asn Ile
105             285                 290                 295
107 ttc agg att tcc aac ctt gtt atg tat atc gtc atc att atc cac tgg       963
108 Phe Arg Ile Ser Asn Leu Val Met Tyr Ile Val Ile Ile Ile His Trp
109             300                 305                 310
111 aat gca tgt gtg ttc tac tct att tct aaa gct att gga ttt gga aat      1011
112 Asn Ala Cys Val Phe Tyr Ser Ile Ser Lys Ala Ile Gly Phe Gly Asn
113     315                 320                 325
115 gat aca tgg gtc .tac cct gat att aat gat cct gaa ttt ggc cgt ttg      1059
116 Asp Thr Trp Val Tyr Pro Asp Ile Asn Asp Pro Glu Phe Gly Arg Leu
117 330                 335                 340                 345
119 gct aga aaa tac gta tac agc ctt tac tgg tct aca ctg act ttg act      1107
120 Ala Arg Lys Tyr Val Tyr Ser Leu Tyr Trp Ser Thr Leu Thr Leu Thr
121                 350                 355                 360
123 acc att ggt gaa aca ccc cct ccc gtg agg gat tct gag tat gtc ttt      1155
124 Thr Ile Gly Glu Thr Pro Pro Pro Val Arg Asp Ser Glu Tyr Val Phe
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·125              365                  370                  375
127 gtg gtg gtt gat ttc cta att gga gtg tta att ttt gct acc atc gtt    1203
128 Val Val Val Asp Phe Leu Ile Gly Val Leu Ile Phe Ala Thr Ile Val
129          380                  385          .        390
131 ggt aac ata ggt tct atg att tcc aac atg aat gca gcc aga gca gaa    1251
132 Gly Asn Ile Gly Ser Met Ile Ser Asn Met Asn Ala Ala Arg Ala Glu
133          395                  400                  405
135 ttt caa gca aga att gat gct atc aag caa tat atg cat ttt cga aat    1299
136 Phe Gln Ala Arg Ile Asp Ala Ile Lys Gln Tyr Met His Phe Arg Asn
137 410                  415                  420                  425
139 gta agc aaa gat atg gaa aag agg gtt att aaa tgg ttt gac tac ctg    1347
140 Val Ser Lys Asp Met Glu Lys Arg Val Ile Lys Trp Phe Asp Tyr Leu
141          430                  435                  440
143 tgg acc aac aaa aaa aca gtt gat gag aaa gaa gtc tta aag tat cta    1395
144 Trp Thr Asn Lys Lys Thr Val Asp Glu Lys Glu Val Leu Lys Tyr Leu
145          445                  450                  455
147 cct gat aaa cta aga gca gaa att gcc atc aac gtt cac tta gac aca    1443
148 Pro Asp Lys Leu Arg Ala Glu Ile Ala Ile Asn Val His Leu Asp Thr
149          460                  465                  470
151 tta aaa aag gta cgc att ttt gct gat tgt gaa gct ggt ctg ttg gtg    1491
152 Leu Lys Lys Val Arg Ile Phe Ala Asp Cys Glu Ala Gly Leu Leu Val
153          475                  480                  485
155 gag ttg gtc ttg aaa ttg caa ccc caa gtc tac agt cct gga gat tat    1539
156 Glu Leu Val Leu Lys Leu Gln Pro Gln Val Tyr Ser Pro Gly Asp Tyr
157 490                  495                  500          .        505       .
159 att tgc aag aaa ggg gat atc gga cga gag atg tac att atc aag gaa    1587
160 Ile Cys Lys Lys Gly Asp Ile Gly Arg Glu Met Tyr Ile Ile Lys Glu
161          510                  515                  520
163 ggc aaa ctc gct gtg gtg gca gat gat gga gtc act cag ttt gtg gta    1635
164 Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr Gln Phe Val Val
165          525                  530                  535
167 ttg agc gat ggc agc acc ttc ggt gag atc agc att ctt aac att aaa    1683
168 Leu Ser Asp Gly Ser Thr Phe Gly Glu Ile Ser Ile Leu Asn Ile Lys
169          540                  545                  550
171 ggg agc aaa gct ggc aat cga aga acg gcc aat att aaa agt att ggc    1731
172 Gly Ser Lys Ala Gly Asn Arg Arg Thr Ala Asn Ile Lys Ser Ile Gly
173          555                  560                  565
175 tac tca gac ctg ttc tgt ctc tca aaa gat gac ctc atg gaa gct cta    1779
176 Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu Met Glu Ala Leu
177 570                  575                  580          .        585
179 act gag tac cca gat gcc aaa act atg cta gaa gaa aaa ggg aag caa    1827
180 Thr Glu Tyr Pro Asp Ala Lys Thr Met Leu Glu Glu Lys Gly Lys Gln
181          590          .        595                  600
183 att tta atg aaa gat ggt cta ctg gat cta aac att gca aat gct ggc    1875
184 Ile Leu Met Lys Asp Gly Leu Leu Asp Leu Asn Ile Ala Asn Ala Gly
185          605                  610                  615
187 agt gat cct aaa gat ctt gaa gag aag gtt act cga atg gag ggg tca    1923
188 Ser Asp Pro Lys Asp Leu Glu Glu Lys Val Thr Arg Met Glu Gly Ser
189          620                  625                  630
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191 gta gac ctc ctg caa acc agg ttt gcc cga atc ttg gct gag tat gag    1971
192 Val Asp Leu Leu Gln Thr Arg Phe Ala Arg Ile Leu Ala Glu Tyr Glu
193     635             640             645
195 tcc atg cag cag aaa ctg aaa caa aga tta acc aag gtt gag aaa ttt    2019
196 Ser Met Gln Gln Lys Leu Lys Gln Arg Leu Thr Lys Val Glu Lys Phe
197 650             655             660             665
199 ctg aaa ccg ctt att gac aca gaa ttt tca agt att gag gga cct tgg    2067
200 Leu Lys Pro Leu Ile Asp Thr Glu Phe Ser Ser Ile Glu Gly Pro Trp
201             670             675             680
203 agc gaa agt ggg ccc atc gac tct aca tag aaccgaaaag ctggtcatta      2117
204 Ser Glu Ser Gly Pro Ile Asp Ser Thr
205             685             690
207 acagggacat gcctcatgat ccttttgatc ctatgactga catcaactaa aatttaaaag  2177
209 aagaggaaga ctcagttggg aaatttttcc atgaggaaaa tgtgctttgg tgcaaggtac  2237
211 agcccacacc tctctgagag atactatgat taaaaaagct ttatatctgg gattttttcac 2297
213 aactgataat gtgcaaagat ataaactgat taacttgtca gtgtctgtat tttctgattt  2357
215 tttcacatac gctcatttta tgtaatattc ttcataaaaa tgaataagta gccctcactt  2417
217 tcatgccatt tccattgttg agtgaagcgt atttgaagta actgagaatt accatgtaca  2477
219 tcatatttgg gataacattt tta                                          2500
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223 <211> LENGTH: 690
224 <212> TYPE: PRT
225 <213> ORGANISM: homo sapiens
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234             20              25              30
237 Arg Met Glu Asn Gly Ala Cys Ser Ser Phe Ser Glu Asp Asp Asp Ser
238         35              40              45
241 Ala Tyr Thr Ser Glu Glu Ser Glu Asn Glu Asn Pro His Ala Arg Gly
242     50              55              60
245 Ser Phe Ser Tyr Lys Ser Leu Arg Lys Gly Gly Pro Ser Gln Arg Glu
246 65              70              75              80
249 Gln Tyr Leu Pro Gly Ala Ile Ala Ile Phe Asn Val Asn Asn Ser Ser
250             85              90              95
253 Asn Lys Asp Gln Glu Pro Glu Glu Lys Lys Lys Lys Lys Glu Lys
254         100             105             110
257 Lys Ser Lys Ser Asp Asp Lys Asn Glu Asn Lys Asn Asp Pro Glu Lys
258         115             120             125
261 Lys Lys Lys Lys Lys Asp Lys Glu Lys Lys Lys Lys Glu Glu Lys Ser
262     130             135             140
265 Lys Asp Lys Lys Glu His His Lys Lys Glu Val Val Val Ile Asp Pro
266 145             150             155             160
269 Ser Gly Asn Thr Tyr Tyr Asn Trp Leu Phe Cys Ile Thr Leu Pro Val
270             165             170             175
273 Met Tyr Asn Trp Thr Met Val Ile Ala Arg Ala Cys Phe Asp Glu Leu
274             180             185             190
277 Gln Ser Asp Tyr Leu Glu Tyr Trp Leu Ile Leu Asp Tyr Val Ser Asp
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278         195                    200                    205
281 Ile Val Tyr Leu Ile Asp Met Phe Val Arg Thr Arg Thr Gly Tyr Leu
282     210                    215                    220
285 Glu Gln Gly Leu Leu Val Lys Glu Glu Leu Lys Leu Ile Asn Lys Tyr
286 225                    230                    235                    240
289 Lys Ser Asn Leu Gln Phe Lys Leu Asp Val Leu Ser Leu Ile Pro Thr
290                    245                    250                    255
293 Asp Leu Leu Tyr Phe Lys Leu Gly Trp Asn Tyr Pro Glu Ile Arg Leu
294                    260                    265                    270
297 Asn Arg Leu Leu Arg Phe Ser Arg Met Phe Glu Phe Phe Gln Arg Thr
298         275                    280                    285
301 Glu Thr Arg Thr Asn Tyr Pro Asn Ile Phe Arg Ile Ser Asn Leu Val
302         290                    295                    300
305 Met Tyr Ile Val Ile Ile Ile His Trp Asn Ala Cys Val Phe Tyr Ser
306 305                    310                    315                    320
309 Ile Ser Lys Ala Ile Gly Phe Gly Asn Asp Thr Trp Val Tyr Pro Asp
310                    325                    330                    335
313 Ile Asn Asp Pro Glu Phe Gly Arg Leu Ala Arg Lys Tyr Val Tyr Ser
314         340                    345                    350
317 Leu Tyr Trp Ser Thr Leu Thr Leu Thr Thr Ile Gly Glu Thr Pro Pro
318         355                    360                    365
321 Pro Val Arg Asp Ser Glu Tyr Val Phe Val Val Val Asp Phe Leu Ile
322         370                    375                    380
325 Gly Val Leu Ile Phe Ala Thr Ile Val Gly Asn Ile Gly Ser Met Ile
326 385                    390                    395                    400
329 Ser Asn Met Asn Ala Ala Arg Ala Glu Phe Gln Ala Arg Ile Asp Ala
330                    405                    410                    415
333 Ile Lys Gln Tyr Met His Phe Arg Asn Val Ser Lys Asp Met Glu Lys
334         420                    425                    430
337 Arg Val Ile Lys Trp Phe Asp Tyr Leu Trp Thr Asn Lys Lys Thr Val
338         435                    440                    445
341 Asp Glu Lys Glu Val Leu Lys Tyr Leu Pro Asp Lys Leu Arg Ala Glu
342         450                    455                    460
345 Ile Ala Ile Asn Val His Leu Asp Thr Leu Lys Lys Val Arg Ile Phe
346 465                    470                    475                    480
349 Ala Asp Cys Glu Ala Gly Leu Leu Val Glu Leu Val Leu Lys Leu Gln
350                    485                    490                    495
353 Pro Gln Val Tyr Ser Pro Gly Asp Tyr Ile Cys Lys Lys Gly Asp Ile
354         500                    505                    510
357 Gly Arg Glu Met Tyr Ile Ile Lys Glu Gly Lys Leu Ala Val Val Ala
358         515                    520                    525
361 Asp Asp Gly Val Thr Gln Phe Val Val Leu Ser Asp Gly Ser Thr Phe
362         530                    535                    540
365 Gly Glu Ile Ser Ile Leu Asn Ile Lys Gly Ser Lys Ala Gly Asn Arg
366 545                    550                    555                    560
369 Arg Thr Ala Asn Ile Lys Ser Ile Gly Tyr Ser Asp Leu Phe Cys Leu
370                    565                    570                    575
373 Ser Lys Asp Asp Leu Met Glu Ala Leu Thr Glu Tyr Pro Asp Ala Lys
374         580                    585                    590
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/27/2004
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Output Set: **N:\CRF4\10272004\J511657.raw**

<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

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Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\10272004\J511657.raw**

L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date